



LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: ANDERTON, STEPHEN MARK  
VAN DER ZEE, RUURD  
VAN EDEN, WILLEM

(ii) TITLE OF INVENTION: PEPTIDE FRAGMENTS OF MICROBIAL STRESS  
PROTEINS AND PHARMACEUTICAL COMPOSITION MADE THEREOF FOR THE  
TREATMENT AND PREVENTION OF INFLAMMATORY DISEASES

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: THE WEBB LAW FIRM

(B) STREET: 700 KOPPERS BUILDING, 436 SEVENTH AVENUE

(C) CITY: PITTSBURGH

(D) STATE: PENNSYLVANIA

(E) COUNTRY: UNITED STATES OF AMERICA

(F) ZIP: 15219-1818

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5" FLOPPY DISK

(B) COMPUTER: DIGITAL VENTURIS GL 6200

(C) OPERATING SYSTEM: DOS

(D) SOFTWARE: MICROSOFT WORD 2.0c

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/716,169

(B) FILING DATE: 18-SEP-1996

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/NL95/00108

(B) FILING DATE: 21-MAR-1995

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 540

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: UNKNOWN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Met	Ala	Lys	Thr	Ile	Ala	Tyr	Asp	Glu	Glu	Ala	Arg	Arg	Gly	Leu
1				5					10					15
Glu	Arg	Gly	Leu	Asn	Ala	Leu	Ala	Asp	Ala	Val	Lys	Val	Thr	Leu
			20						25					30
Gly	Pro	Lys	Gly	Arg	Asn	Val	Val	Leu	Glu	Lys	Lys	Trp	Gly	Ala
			35						40					45
Pro	Thr	Ile	Thr	Asn	Asp	Gly	Val	Ser	Ile	Ala	Lys	Glu	Ile	Glu
			50						55					60
Leu	Glu	Asp	Pro	Tyr	Glu	Lys	Ile	Gly	Ala	Glu	Leu	Val	Lys	Glu
			65						70					75
Val	Ala	Lys	Lys	Thr	Asp	Asp	Val	Ala	Gly	Asp	Gly	Thr	Thr	Thr
			80						85					90

Ala Thr Val Leu Ala Gln Ala Leu Val Arg Glu Gly Leu Arg Asn  
95 100 105

Val Ala Ala Gly Ala Asn Pro Leu Gly Val Lys Arg Gly Ile Glu  
110 115 120

Lys Ala Val Glu Lys Val Thr Glu Thr Leu Leu Lys Gly Ala Lys  
125 130 135

Glu Val Glu Thr Lys Glu Gln Ile Ala Ala Thr Ala Ala Ile Ser  
140 145 150

Ala Gly Asp Gln Ser Ile Gly Asp Leu Ile Ala Glu Ala Met Asp  
155 160 165

Lys Val Gly Asn Glu Gly Val Ile Thr Val Glu Glu Ser Asn Thr  
170 175 180

Phe Gly Leu Gln Leu Glu Leu Thr Glu Gly Met Arg Phe Asp Lys  
185 190 195

Gly Tyr Ile Ser Gly Tyr Phe Val Thr Asp Pro Glu Arg Gln Glu  
200 205 210

Ala Val Leu Glu Asp Pro Tyr Ile Leu Leu Val Ser Ser Lys Val  
215 220 225

Ser Thr Val Lys Asp Leu Leu Pro Leu Leu Glu Lys Val Ile Gly  
230 235 240

Ala Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Val Glu Gly Glu  
245 250 255

Ala Leu Ser Thr Leu Val Val Asn Lys Ile Arg Gly Thr Phe Lys  
260 265 270

Ser Val Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala  
275 280 285

Met Leu Gln Asp Met Ala Ile Leu Thr Gly Gly Gln Val Ile Ser  
290 295 300

Glu Glu Val Gly Leu Thr Leu Glu Asn Ala Asp Leu Ser Leu Leu  
305 310 315

Gly Lys Ala Arg Lys Val Val Val Thr Lys Asp Glu Thr Thr Ile  
320 325 330

Val Glu Gly Ala Gly Asp Thr Asp Ala Ile Ala Gly Arg Val Ala  
335 340 345

Gln Ile Arg Gln Glu Ile Glu Asn Ser Asp Ser Asp Tyr Asp Arg  
 350 355 360  
 Glu Lys Leu Gln Glu Arg Leu Ala Lys Leu Ala Gly Gly Val Ala  
 365 370 375  
 Val Ile Lys Ala Gly Ala Ala Thr Glu Val Glu Leu Lys Glu Arg  
 380 385 390  
 Lys His Arg Ile Glu Asp Ala Val Arg Asn Ala Lys Ala Ala Val  
 395 400 405  
 Glu Glu Gly Ile Val Ala Gly Gly Gly Val Thr Leu Leu Gln Ala  
 410 415 420  
 Ala Pro Thr Leu Asp Glu Leu Lys Leu Glu Gly Asp Glu Ala Thr  
 425 430 435  
 Gly Ala Asn Ile Val Lys Val Ala Leu Glu Ala Pro Leu Lys Gln  
 440 445 450  
 Ile Ala Phe Asn Ser Gly Leu Glu Pro Gly Val Val Ala Glu Lys  
 455 460 465  
 Val Arg Asn Leu Pro Ala Gly His Gly Leu Asn Ala Gln Thr Gly  
 470 475 480  
 Val Lys Glu Asp Leu Leu Ala Ala Gly Val Ala Asp Pro Val Lys  
 485 490 495  
 Val Thr Arg Ser Ala Leu Gln Asn Ala Ala Ser Ile Ala Gly Leu  
 500 505 510  
 Phe Leu Thr Thr Glu Ala Val Val Ala Asp Lys Pro Glu Lys Glu  
 515 520 525  
 Lys Ala Ser Val Pro Gly Gly Gly Asp Met Gly Gly Met Asp Phe  
 530 535 540

(3) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 333

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: UNKNOWN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Ala Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Asn  
 1 5 10 15  
 Val Phe Arg Ala Ala Leu Lys Asn Pro Asp Ile Glu Val Val Ala  
 20 25 30

Val Asn Asp Leu Thr Asp Ala Asn Thr Leu Ala His Leu Leu Lys  
 35 40 45  
 Tyr Asp Ser Val His Gly Arg Leu Asp Ala Glu Val Ser Val Asn  
 50 55 60  
 Gly Asn Asn Leu Val Val Asn Gly Lys Glu Ile Ile Val Lys Ala  
 65 70 75  
 Glu Arg Asp Pro Glu Asn Leu Ala Trp Gly Glu Ile Gly Val Asp  
 80 85 90  
 Ile Val Val Glu Ser Thr Gly Arg Phe Thr Lys Arg Glu Asp Ala  
 95 100 105  
 Ala Lys His Leu Glu Ala Gly Ala Lys Lys Val Ile Ile Ser Ala  
 110 115 120  
 Pro Ala Lys Asn Glu Asp Ile Thr Ile Val Met Gly Val Asn Gln  
 125 130 135  
 Asp Lys Tyr Asp Pro Lys Ala His His Val Ile Ser Asn Ala Ser  
 140 145 150  
 Cys Thr Thr Asn Cys Leu Ala Pro Phe Ala Lys Val Leu His Glu  
 155 160 165  
 Gln Phe Gly Ile Val Arg Gly Met Met Thr Thr Val His Ser Tyr  
 170 175 180  
 Thr Asn Asp Gln Arg Ile Leu Asp Leu Pro His Lys Asp Leu Arg  
 185 190 195  
 Arg Ala Arg Ala Ala Ala Glu Ser Ile Ile Pro Thr Thr Thr Gly  
 200 205 210  
 Ala Ala Lys Ala Val Ala Leu Val Leu Pro Glu Leu Lys Gly Lys  
 215 220 225  
 Leu Asn Gly Met Ala Met Arg Val Pro Thr Pro Asn Val Ser Val  
 230 235 240  
 Val Asp Leu Val Ala Glu Leu Glu Lys Glu Val Thr Val Glu Glu  
 245 250 255  
 Val Asn Ala Ala Leu Lys Ala Ala Ala Glu Gly Glu Leu Lys Gly  
 260 265 270  
 Ile Leu Ala Tyr Ser Glu Glu Pro Leu Val Ser Arg Asp Tyr Asn  
 275 280 285

Gly Ser Thr Val Ser Ser Thr Ile Asp Ala Leu Ser Thr Met Val  
290 295 300

Ile Asp Gly Lys Met Val Lys Val Val Ser Trp Tyr Asp Asn Glu  
305 310 315

Thr Gly Tyr Ser His Arg Val Val Asp Leu Ala Ala Tyr Ile Ala  
320 325 330

Ser Lys Gly

(4) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 332

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: UNKNOWN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Val Lys Val Gly Val Asn Gly Phe Gly Arg Ile Gly Arg Leu Val  
1 5 10 15

Thr Arg Ala Ala Phe Ser Cys Asp Lys Val Asp Ile Val Ala Ile  
20 25 30

Asn Asp Pro Phe Ile Asp Leu Asn Tyr Met Val Tyr Met Phe Gln  
35 40 45

Tyr Asp Ser Thr His Gly Lys Phe Asn Gly Thr Val Lys Ala Glu  
50 55 60

Asn Gly Lys Leu Val Ile Asn Gly Lys Pro Ile Thr Ile Phe Gln  
65 70 75

Glu Arg Asp Pro Val Lys Ile Lys Trp Gly Asp Ala Gly Ala Glu  
80 85 90

Tyr Val Val Glu Ser Thr Gly Val Phe Thr Thr Met Glu Lys Ala  
95 100 105

Gly Ala His Leu Lys Gly Gly Ala Lys Arg Val Ile Ile Ser Ala  
110 115 120

Pro Ser Ala Asp Ala Pro Met Phe Val Met Gly Val Asn His Glu  
125 130 135

Lys Tyr Asp Asn Ser Leu Lys Ile Val Ser Asn Ala Ser Cys Thr  
140 145 150

Thr Asn Cys Leu Ala Pro Leu Ala Lys Val Ile His Asp Asn Phe  
155 160 165

Gly Ile Val Glu Gly Leu Met Thr Thr Val His Ala Ile Thr Ala 180  
 170  
 Thr Gln Lys Thr Val Asp Gly Pro Ser Gly Lys Leu Trp Arg Asp 195  
 185  
 Gly Arg Gly Ala Ala Gln Asn Ile Ile Pro Ala Ser Thr Gly Ala 210  
 200  
 Ala Lys Ala Val Gly Lys Val Ile Pro Glu Leu Asn Gly Lys Leu 225  
 215  
 Thr Gly Met Ala Phe Arg Val Pro Thr Pro Asn Val Ser Val Val 240  
 230  
 Asp Leu Thr Cys Arg Leu Glu Lys Pro Ala Lys Tyr Asp Asp Ile 255  
 245  
 Lys Lys Val Val Lys Gln Ala Ala Glu Gly Pro Leu Lys Gly Ile 270  
 260  
 Leu Gly Tyr Thr Glu Asp Gln Val Val Ser Cys Asp Phe Asn Ser 285  
 275  
 Asn Ser His Ser Ser Thr Phe Asp Ala Gly Ala Gly Ile Ala Leu 300  
 290  
 Asn Asp Asn Ile Val Lys Leu Ile Ser Trp Tyr Asp Asn Glu Tyr 315  
 305  
 Gly Tyr Ser Asn Arg Val Val Asp Leu Met Ala Tyr Met Ala Ser 330  
 320  
 Lys Glu

(5) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 573

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: UNKNOWN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Leu Arg Leu Pro Thr Val Phe Arg Gln Met Arg Pro Val Ser 15  
 1 5 10

Arg Val Leu Ala Pro His Leu Thr Arg Ala Tyr Ala Lys Asp Val 30  
 20 25

Lys Phe Gly Ala Asp Ala Arg Ala Leu Met Leu Gln Gly Val Asp 45  
 35 40

Leu Leu Ala Asp Ala Val Ala Val Thr Met Gly Pro Lys Gly Arg  
 50 55 60  
 Thr Val Ile Ile Glu Gln Ser Trp Gly Ser Pro Lys Val Thr Lys  
 65 70 75  
 Asp Gly Val Thr Val Ala Lys Ser Ile Asp Leu Lys Asp Lys Tyr  
 80 85 90  
 Lys Asn Ile Gly Ala Lys Leu Val Gln Asp Val Ala Asn Asn Thr  
 95 100 105  
 Asn Glu Glu Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala  
 110 115 120  
 Arg Ser Ile Ala Lys Glu Gly Phe Glu Lys Ile Ser Lys Gly Ala  
 125 130 135  
 Asn Pro Val Glu Ile Arg Arg Gly Val Met Leu Ala Val Asp Ala  
 140 145 150  
 Val Ile Ala Glu Leu Lys Lys Gln Ser Lys Pro Val Thr Thr Pro  
 155 160 165  
 Glu Glu Ile Ala Gln Val Ala Thr Ile Ser Ala Asn Gly Asp Lys  
 170 175 180  
 Glu Ile Gly Asn Ile Ile Ser Asp Ala Met Lys Lys Val Gly Arg  
 185 190 195  
 Lys Gly Val Ile Thr Val Lys Asp Gly Lys Thr Leu Asn Asp Glu  
 200 205 210  
 Leu Glu Ile Ile Glu Gly Met Lys Phe Asp Arg Gly Tyr Ile Ser  
 215 220 225  
 Pro Tyr Phe Ile Asn Thr Ser Lys Gly Gln Lys Cys Glu Phe Gln  
 230 235 240  
 Asp Ala Tyr Val Leu Leu Ser Glu Lys Lys Ile Ser Ser Ile Gln  
 245 250 255  
 Ser Ile Val Pro Ala Leu Glu Ile Ala Asn Ala His Arg Lys Pro  
 260 265 270  
 Leu Val Ile Ile Ala Glu Asp Val Asp Gly Glu Ala Leu Ser Thr  
 275 280 285  
 Leu Val Leu Asn Arg Leu Lys Val Gly Leu Gln Val Val Ala Val  
 290 295 300

Lys Ala Pro Gly Phe Gly Asp Asn Arg Lys Asn Gln Leu Lys Asp 315  
 305 310  
 Met Ala Ile Ala Thr Gly Gly Ala Val Phe Gly Glu Glu Gly Leu 330  
 320 325  
 Thr Leu Asn Leu Glu Asp Val Gln Pro His Asp Leu Gly Lys Val 345  
 335 340  
 Gly Glu Val Ile Val Thr Lys Asp Asp Ala Met Leu Leu Lys Gly 360  
 350 355  
 Lys Gly Asp Lys Ala Gln Ile Glu Lys Arg Ile Gln Glu Ile Ile 375  
 365 370  
 Glu Gln Leu Asp Val Thr Thr Ser Glu Tyr Glu Lys Glu Lys Leu 390  
 380 385  
 Asn Glu Arg Leu Ala Lys Leu Ser Asp Gly Val Ala Val Leu Lys 405  
 395 400  
 Val Gly Gly Thr Ser Asp Val Glu Val Asn Glu Lys Lys Asp Arg 420  
 410 415  
 Val Thr Asp Ala Leu Asn Ala Thr Arg Ala Ala Val Glu Glu Gly 435  
 425 430  
 Ile Val Leu Gly Gly Gly Cys Ala Leu Leu Arg Cys Ile Pro Ala 450  
 440 445  
 Leu Asp Ser Leu Thr Pro Ala Asn Glu Asp Gln Lys Ile Gly Ile 465  
 455 460  
 Glu Ile Ile Lys Arg Thr Leu Lys Ile Pro Ala Met Thr Ile Ala 480  
 470 475  
 Lys Asn Ala Gly Val Glu Gly Ser Leu Ile Val Glu Lys Ile Met 495  
 485 490  
 Gln Ser Ser Ser Glu Val Gly Tyr Asp Ala Met Ala Gly Asp Phe 510  
 500 505  
 Val Asn Met Val Glu Lys Gly Ile Ile Asp Pro Thr Lys Val Val 525  
 515 520  
 Arg Thr Ala Leu Leu Asp Ala Ala Gly Val Ala Ser Leu Leu Thr 540  
 530 535  
 Thr Ala Glu Val Val Val Thr Glu Ile Pro Lys Glu Glu Lys Asp 555  
 545 550



Pro Gly Met Gly Ala Met Gly Gly Met Gly Gly Gly Met Gly Gly  
560 565 570

Gly Met Phe

(6) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 547

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: UNKNOWN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Ala	Lys	Asp	Val	Lys	Phe	Gly	Ala	Asp	Ala	Arg	Ala	Leu	Met	Leu	1	5	10	15
Gln	Gly	Val	Asp	Leu	Leu	Ala	Asp	Ala	Val	Ala	Val	Thr	Met	Gly	20	25	30	
Pro	Lys	Gly	Arg	Thr	Val	Ile	Ile	Glu	Gln	Ser	Trp	Gly	Ser	Pro	35	40	45	
Lys	Val	Thr	Lys	Asp	Gly	Val	Thr	Val	Ala	Lys	Ser	Ile	Asp	Leu	50	55	60	
Lys	Asp	Lys	Tyr	Lys	Asn	Ile	Gly	Ala	Lys	Leu	Val	Gln	Asp	Val	65	70	75	
Ala	Asn	Asn	Thr	Asn	Glu	Glu	Ala	Gly	Asp	Gly	Thr	Thr	Thr	Ala	80	85	90	
Thr	Val	Leu	Ala	Arg	Ser	Ile	Ala	Lys	Glu	Gly	Phe	Glu	Lys	Ile	95	100	105	
Ser	Lys	Gly	Ala	Asn	Pro	Val	Glu	Ile	Arg	Arg	Gly	Val	Met	Leu	110	115	120	
Ala	Val	Asp	Ala	Val	Ile	Ala	Glu	Leu	Lys	Lys	Gln	Ser	Lys	Pro	125	130	135	
Val	Thr	Thr	Pro	Glu	Glu	Ile	Ala	Gln	Val	Ala	Thr	Ile	Ser	Ala	140	145	150	
Asn	Gly	Asp	Lys	Asp	Ile	Gly	Asn	Ile	Ile	Ser	Asp	Ala	Met	Lys	155	160	165	
Lys	Val	Gly	Arg	Lys	Gly	Val	Ile	Thr	Val	Lys	Asp	Gly	Lys	Thr	170	175	180	
Leu	Asn	Asp	Glu	Leu	Glu	Ile	Ile	Glu	Gly	Met	Lys	Phe	Asp	Arg	185	190	195	

Gly Tyr Ile Ser Pro Tyr Phe Ile Asn Thr Ser Lys Gly Gln Lys  
 200 205 210  
 Cys Glu Phe Gln Asp Ala Tyr Val Leu Leu Ser Glu Lys Lys Ile  
 215 220 225  
 Ser Ser Val Gln Ser Ile Val Pro Ala Leu Glu Ile Ala Asn Ala  
 230 235 240  
 His Arg Lys Pro Leu Val Ile Ile Ala Glu Asp Val Asp Gly Glu  
 245 250 255  
 Ala Leu Ser Thr Leu Val Leu Asn Arg Leu Lys Val Gly Leu Gln  
 260 265 270  
 Val Val Ala Val Lys Ala Pro Gly Phe Gly Asp Asn Arg Lys Asn  
 275 280 285  
 Gln Leu Lys Asp Met Ala Ile Ala Thr Gly Gly Ala Val Phe Gly  
 290 295 300  
 Glu Glu Gly Leu Asn Leu Asn Leu Glu Asp Val Gln Ala His Asp  
 305 310 315  
 Leu Gly Lys Val Gly Glu Val Ile Val Thr Lys Asp Asp Ala Met  
 320 325 330  
 Leu Leu Lys Gly Lys Gly Asp Lys Ala His Ile Glu Lys Arg Ile  
 335 340 345  
 Gln Glu Ile Thr Glu Gln Leu Asp Ile Thr Thr Ser Glu Tyr Glu  
 350 355 360  
 Lys Glu Lys Leu Asn Glu Arg Leu Ala Lys Leu Ser Asp Gly Val  
 365 370 375  
 Ala Val Leu Lys Val Gly Gly Thr Ser Asp Val Glu Val Asn Glu  
 380 385 390  
 Lys Lys Asp Arg Val Thr Asp Ala Leu Asn Ala Thr Arg Ala Ala  
 395 400 405  
 Val Glu Glu Gly Ile Val Leu Gly Gly Gly Cys Ala Leu Leu Arg  
 410 415 420  
 Cys Ile Pro Ala Leu Asp Ser Leu Lys Pro Ala Asn Glu Asp Gln  
 425 430 435  
 Lys Ile Gly Ile Glu Ile Ile Lys Arg Ala Leu Lys Ile Pro Ala  
 440 445 450

Met Thr Ile Ala Lys Asn Ala Gly Val Glu Gly Ser Leu Ile Val  
455 460 465

Glu Lys Ile Leu Gln Ser Ser Ser Glu Val Gly Tyr Asp Ala Met  
470 475 480

Leu Gly Asp Phe Val Asn Met Val Glu Lys Gly Ile Ile Asp Pro  
485 490 495

Thr Lys Val Val Arg Thr Ala Leu Leu Asp Ala Ala Gly Val Ala  
500 505 510

Ser Leu Leu Thr Thr Ala Glu Ala Val Val Thr Glu Ile Pro Lys  
515 520 525

Glu Glu Lys Asp Pro Gly Met Gly Ala Met Gly Gly Met Gly Gly  
530 535 540

Gly Met Gly Gly Gly Met Phe  
545

(7) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 555

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: UNKNOWN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Ala Pro His Leu Thr Arg Ala Tyr Ala Lys Asp Val Lys Phe Gly  
1 5 10 15

Ala Asp Ala Arg Ala Leu Met Leu Gln Gly Val Asp Leu Leu Ala  
20 25 30

Asp Ala Val Ala Val Thr Met Gly Pro Lys Gly Arg Thr Val Ile  
35 40 45

Ile Glu Gln Ser Trp Gly Ser Pro Lys Val Thr Lys Asp Gly Val  
50 55 60

Thr Val Ala Lys Ser Ile Asp Leu Lys Asp Lys Tyr Lys Asn Ile  
65 70 75

Gly Ala Lys Leu Val Gln Asp Val Ala Asn Asn Thr Asn Glu Glu  
80 85 90

Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Arg Ser Ile  
95 100 105

Ala Lys Glu Gly Phe Glu Lys Ile Ser Lys Gly Ala Asn Pro Val  
110 115 120

Glu Ile Arg Arg Gly Val Met Leu Ala Val Asp Ala Val Ile Ala 135  
 125 130  
 Glu Leu Lys Lys Gln Ser Lys Pro Val Thr Thr Pro Glu Glu Ile 150  
 140 145  
 Ala Gln Val Ala Thr Ile Ser Ala Asn Gly Asp Lys Asp Ile Gly 165  
 155 160  
 Asn Ile Ile Ser Asp Ala Met Lys Lys Val Gly Arg Lys Gly Val 180  
 170 175  
 Ile Thr Val Lys Asp Gly Lys Thr Leu Asn Asp Glu Leu Glu Ile 195  
 185 190  
 Ile Glu Gly Met Lys Phe Asp Arg Gly Tyr Ile Ser Pro Tyr Phe 210  
 200 205  
 Ile Asn Thr Ser Lys Gly Gln Lys Cys Glu Phe Gln Asp Ala Tyr 225  
 215 220  
 Val Leu Leu Ser Glu Lys Lys Phe Ser Ser Val Gln Ser Ile Val 240  
 230 235  
 Pro Ala Leu Glu Ile Ala Asn Ala His Arg Lys Pro Leu Val Ile 255  
 245 250  
 Ile Ala Glu Asp Val Asp Gly Glu Ala Leu Ser Thr Leu Val Leu 270  
 260 265  
 Asn Arg Leu Lys Val Gly Leu Gln Val Val Ala Val Lys Ala Pro 285  
 275 280  
 Gly Phe Gly Asp Asn Arg Lys Asn Gln Leu Lys Asp Met Ala Ile 300  
 290 295  
 Ala Thr Gly Gly Ala Val Phe Gly Glu Glu Gly Leu Asn Leu Asn 315  
 305 310  
 Leu Glu Asp Val Gln Ala His Asp Leu Gly Lys Val Gly Glu Val 330  
 320 325  
 Ile Val Thr Lys Asp Asp Ala Met Leu Leu Lys Gly Lys Gly Asp 345  
 335 340  
 Lys Ala His Ile Glu Lys Arg Ile Gln Glu Ile Thr Glu Gln Leu 360  
 350 355  
 Asp Ile Thr Thr Ser Glu Tyr Glu Lys Glu Lys Leu Asn Glu Arg 375  
 365 370

Leu Ala Lys Leu Ser Asp Gly Val Ala Val Leu Lys Val Gly Gly  
 380 385 390  
 Thr Ser Asp Val Glu Val Asn Glu Lys Lys Asp Arg Val Thr Asp  
 395 400 405  
 Ala Leu Asn Ala Thr Arg Ala Ala Val Glu Glu Gly Ile Val Leu  
 410 415 420  
 Gly Gly Gly Cys Ala Leu Leu Arg Cys Ile Pro Ala Leu Asp Ser  
 425 430 435  
 Leu Lys Pro Ala Asn Glu Asp Gln Lys Ile Gly Ile Glu Ile Ile  
 440 445 450  
 Lys Arg Ala Leu Lys Ile Pro Ala Met Thr Ile Ala Lys Asn Ala  
 455 460 465  
 Gly Val Glu Gly Ser Leu Ile Val Glu Lys Ile Leu Gln Ser Ser  
 470 475 480  
 Ser Glu Val Gly Tyr Asp Ala Met Leu Gly Asp Phe Val Asn Met  
 485 490 495  
 Val Glu Lys Gly Ile Ile Asp Pro Thr Lys Val Val Arg Thr Ala  
 500 505 510  
 Leu Leu Asp Ala Ala Gly Val Ala Ser Leu Leu Thr Thr Ala Glu  
 515 520 525  
 Ala Val Val Thr Glu Ile Pro Lys Glu Glu Lys Asp Pro Gly Met  
 530 535 540  
 Gly Ala Met Gly Gly Met Gly Gly Gly Met Gly Gly Gly Met Phe  
 545 550 555